

SEQUENCE LISTING

<110> Valenzuela et al.

<120> DORSAL TISSUE AFFECTING FACTOR AND COMPOSITIONS

<130> REG132-B1

<140> Not Yet Known

<141> Filed Herewith

<150> 09/167,874

<151> 1998-10-07

<150> 08/485,721

<151> 1995-07-06

<150> 08/392,935

<151> 1995-09-22

<150> PCT/US93/08326

<151> 1993-09-02

<150> 07/957,401

<151> 1992-10-06

<150> 07/950,410

<151> 1992-09-23

<150> 07/939,954

<151> 1992-09-03

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 699

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(696)

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Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val  
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gtc ctg ggg ctg cgg gcg aca ccg gcc ggc ggc cag cac tat ctc cac 96

D D G G G G E

Val	Leu	Gly	Leu	Arg	Ala	Thr	Pro	Ala	Gly	Gly	Gln	His	Tyr	Leu	His	
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																25
																30
atc	cgc	ccg	gca	ccc	agc	gac	aac	ctg	ccc	ctg	gtg	gac	ctc	atc	gaa	144
Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu	
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																40
																45
cac	cca	gac	cct	atc	ttt	gac	ccc	aag	gaa	aag	gat	ctg	aac	gag	acg	192
His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr	
																50
																55
																60
ctg	ctg	cgc	tcg	ctg	ctc	ggg	ggc	cac	tac	gac	cca	ggc	ttc	atg	gcc	240
Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala	
																65
																70
																75
																80
acc	tcg	ccc	ccc	gag	gac	cgg	ccc	ggg	ggg	ggc	ggg	ggt	gca	gct	ggg	288
Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Gly	
																85
																90
																95
ggc	gcf	gag	gac	ctg	gcf	gag	ctg	gac	cag	ctg	ctg	cgg	cag	cgg	ccg	336
Gly	Ala	Glu	Asp	Leu	Ala	Glu	Leu	Asp	Gln	Leu	Leu	Arg	Gln	Arg	Pro	
																100
																105
																110
tcg	ggg	gcc	atg	ccg	agc	gag	atc	aaa	ggg	cta	gag	ttc	tcc	gag	ggc	384
Ser	Gly	Ala	Met	Pro	Ser	Glu	Ile	Lys	Gly	Leu	Glu	Phe	Ser	Glu	Gly	
																115
																120
																125
ttg	gcc	cag	ggc	aag	aag	cag	cgc	cta	agc	aag	aag	ctg	cgg	agg	aag	432
Leu	Ala	Gln	Gly	Lys	Lys	Gln	Arg	Leu	Ser	Lys	Lys	Leu	Arg	Arg	Lys	
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																135
																140
tta	cag	atg	tgg	ctg	tgg	tcg	cag	aca	ttc	tgc	ccc	gtg	ctg	tac	gcf	480
Leu	Gln	Met	Trp	Leu	Trp	Ser	Gln	Thr	Phe	Cys	Pro	Val	Leu	Tyr	Ala	
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																150
																155
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tgg	aac	gac	ctg	ggc	agc	cgc	ttt	tgg	ccg	cgc	tac	gtg	aag	gtg	ggc	528
Trp	Asn	Asp	Leu	Gly	Ser	Arg	Phe	Trp	Pro	Arg	Tyr	Val	Lys	Val	Gly	
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																170
																175
agc	tgc	tcc	agt	aag	cgc	tcg	tgc	tcc	gtg	ccc	gag	ggc	atg	gtg	tgc	576
Ser	Cys	Phe	Ser	Lys	Arg	Ser	Cys	Ser	Val	Pro	Glu	Gly	Met	Val	Cys	
																180
																185
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aag	ccg	tcc	aag	tcc	gtg	cac	ctc	acg	gtg	ctg	cgg	tgg	cgc	tgt	cag	624
Lys	Pro	Ser	Lys	Ser	Val	His	Leu	Thr	Val	Leu	Arg	Trp	Arg	Cys	Gln	
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																205
cgf	cgc	ggg	ggc	cag	cgc	tgc	ggc	tgg	att	ccc	atc	cag	tac	ccc	atc	672

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile			
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Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu			
35	40	45	
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr			
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Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala			
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Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Ala Ala Gly			
85	90	95	
Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro			
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Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly			
115	120	125	
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys			
130	135	140	
Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala			
145	150	155	160
Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly			
165	170	175	
Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys			

180

185

190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln  
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Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile  
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Ile Ser Glu Cys Lys Cys Ser Cys  
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<210> 4  
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1 5 10

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<212> PRT  
<213> frog and mouse

<400> 5  
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1 5 10

<210> 6  
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Leu Arg Trp Arg Cys Gln Arg Arg

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5

<210> 7

<211> 8

<212> PRT

<213> frog and mouse

<400> 7

Ile Ser Glu Cys Lys Cys Ser Cys

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5

<210> 8

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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36

<210> 9

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

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ccaagttctt agaattcgca ggaacactta cactcg

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<210> 10

<211> 1180

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Yeast genome sequence

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tcgaaaattaa ccctcactaa agggaaacaaa agctggagct ccaccgcgggt ggccggccgcc 180
ttcccaagta gagcggcggg ggggaattgc gaccaactcg tgcgcgtctt ctgcncggcg 240
gcgggagccg gcgctgcgcg aacggctctc ctcgcagctc atgctgcctg ccctgcgcct 300
gctcaggctc gggtgagcca cctccggagg gaccggggag cgccggcagcg ccgcggactc 360
ggcgtgtctt cctccgggggca cgccggacgaa agaggcagcc ccggggcgcg cgccggaggc 420
atg gag cgc tgc ccc agc ctg ggg gtc acc ctc tac gcc ctg gtg gtg 468
Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
    1           5           10          15
gtc ctg ggg ctg cgg gca gca cca gcc ggc ggc cag cac tat cta cac 516
Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
    20          25          30
atc cgc cca gca ccc agc gac aac ctg ccc ttg gtg gac ctc atc gaa 564
Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
    35          40          45
cat cca gac cct atc ttt gac cct aag gag aag gat ctg aac gag acg 612
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
    50          55          60
ctg ctg cgc tcg ctg ctc ggg ggc cac tac gac ccg ggc ttt atg gcc 660
Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
    65          70          75          80
act tcg ccc cca gag gac cga ccc gga ggg ggc ggg gga ccg gct gga 708
Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Pro Ala Gly
    85          90          95
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DRAFT

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Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro  
100 105 110

tcg ggg gcc atg ccg agc gag atc aaa ggg ctg gag ttc tcc gag ggc 804  
Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly  
115 120 125

ttg gcc caa ggc aag aaa cag cgc ctg agc aag aag ctg agg agg aag 852  
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys  
130 135 140

tta cag atg tgg ctg tgg tca cag acc ttc tgc ccg gtg ctg tac gcg 900  
Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala  
145 150 155 160

tgg aat gac cta ggc agc cgc ttt tgg cca cgc tac gtg aag gtg ggc 948  
Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly  
165 170 175

agc tgc ttc agc aag cgc tcc tgc tct gtg ccc gag ggc atg gtg tgt 996  
Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys  
180 185 190

aag cca tcc aag tct gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag 1044  
Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln  
195 200 205

cgg cgc ggg ggt cag cgc tgc ggc tgg att ccc atc cag tac ccc atc 1092  
Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile  
210 215 220

att tcc gag tgt aag tgt tcc tgc tagaactcg ggccccccc tgcccgccc 1146  
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225 230

cagacacttg atggatcccc cgggctgaga tttt 1180

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1 5 10 15

Sequence Database Search Results

Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His  
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Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu  
35 40 45

His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr  
50 55 60

Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala  
65 70 75 80

Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Pro Ala Gly  
85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro  
100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly  
115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys  
130 135 140

Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala  
145 150 155 160

Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly  
165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys  
180 185 190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln  
195 200 205

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile  
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Ile Ser Glu Cys Lys Cys Ser Cys  
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DNA sequence

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